

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=9; day=11; hr=14; min=23; sec=23; ms=624;]

=====

Reviewer Comments:

<210> 23

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> PP2A motif

<220>

<221> misc_feature

<222> (3)..(3)

<223> Xaa can be any naturally occurring amino acid

<400> 23

Gly Asp Xaa His Gly Gln

1 5

Although the above "<211>" response is "7", only 6 amino acids are shown above.

Application No: 10590551 Version No: 3.0

Input Set:

Output Set:

Started: 2009-08-27 18:04:53.801
Finished: 2009-08-27 18:04:55.734
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 933 ms
Total Warnings: 15
Total Errors: 1
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 331	Count of Protein differs from the <211> tag Input: 7 Calculated:
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

SEQUENCE LISTING

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel Phytochrome-interacting protein and a use thereof

<130> OP05-1002

<140> 10590551

<141> 2009-08-27

<150> KR10-2004-0013663

<151> 2004-02-27

<160> 26

<170> KopatentIn 1.71

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 1

ggatccaaat gtcaggctct aggccgact

29

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 2

ctcgagctac ttgttgctg cagcgagttc

30

<210> 3

<211> 1455

<212> DNA

<213> Arabidopsis thaliana

<400> 3

atggagacca agaatgagaa ttctgatgtt tcacggcag aggagttaa aagt caggcc

60

aacgaagctt ttaaaggta caaatactcc agtgctattg atctatatac aaaagctatt

120

gaactcaaca gcaacaacgc tgtgtattgg gcaaatcgtg catttgctca cacaaaactg

180

gaggaaatatg gcagtgcata acaggatgca tcgaaggcca ttgaagttga ttcaagatac 240
tctaagggtt attacaggcg tggtgctgcg tatcttgcca tggaaaatt taaggatgcc 300
ttgaaggact tccaacaggt aaaaaggctt tctcctaattg accctgatgc cacaagaaag 360
ctaaaggaaat gtgagaaagc agtgatgaaa ctcaaatttgc aagaagcaat ctctgtgcca 420
gtatctgaaa ggcgttcagt agctgagtcc attgacttcc atacaataga ggttgagcca 480
caatattctg gtgctagaat tgagggagag gaagttacct tagattttgt gaaaacgatg 540
atggaggatt ttaagaacca aaaaacatttgc cataaacggt atgcctatca aatcgcttta 600
cagacttaggc aaatcttgcg actgcactgcct tctcttgcgttgc atataagtgt tccacatggc 660
aaacatatca ctgtttgcgg tgacgttcat ggtcagttct acgatcttct caatatcttt 720
gagcttaatg gcctcccttc ggaggagaac ccataacctat ttaatggcga ctttggac 780
agaggctcat tctccgttga gatcatcctc actttgttttgc ctttcaagtgc catgtgccc 840
tcatccatat atctagccag agggaaaccat gaaagcaaga gcatgaacaa aatttatggt 900
tttgggggtt aggttcggtc caagttgagt gaaaaattcg tggatcttt tgctgaagtt 960
ttctgttacc tcccggttgc tcatgttata aatggaaagg tcttcgttgtt acatggaggt 1020
ctttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag 1080
ccaccagagg aaggactaat gtgtgaacta ttgtggagtg atcctcaacc tctcccttgg 1140
agaggcccaa gcaagcgagg agttggtcta tcatttgggtt gagatgtgac aaagaggttt 1200
ttgcaagata acaatttgcg tttgttggtc cggtcacatg aagtaaaaga tgaaggttat 1260
gaggttgaac atgacggtaa actcataact gtcttctctg cgccaaatata ctgtgatcag 1320
atgggttaata agggagcctt cattcggtttt gaagctcctg atatgaagcc aaacattttttt 1380
acattctcag cagtgcctca tccggatgtt aagcctatgg catatgcaaa caactttctc 1440
aggatgttca actaa 1455

<210>	4
<211>	484
<212>	PRT
<213>	<i>Arabidopsis thaliana</i>

<400> 4
Met Glu Thr Lys Asn Glu Asn Ser Asp Val Ser Arg Ala Glu Glu Phe
1 5 10 15

Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
 20 25 30

Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95

Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro
100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
225 230 235 240

Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
260 265 270

Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
420 425 430

Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
435 440 445

Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
450 455 460

Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
465 470 475 480

Arg Met Phe Asn

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 5
ggatccatgg agaccaagaa tgag 24

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 6
ctcgagttag ttgaacatcc tgag 24

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
ggatccgatg tcaggctcta ggccgact 28

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
gctgatcagc atggttccg gagtcggggg tagt 34

<210> 9
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 9
cccgccggaa ctaatatggc atcatcagca tcat 34

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 10
ctcgagtcaa gagattgctt cttcaaa 27

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
 <223> PCR primer

<400> 11
 ggatccatgc cagtatctga aaggcgt

27

<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 12
 atggagacca agaatgagaa ttct

24

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 13
 ttagttgaac atcctgagaa agtt

24

<210> 14
 <211> 347
 <212> PRT
 <213> Arabidopsis thaliana

<400> 14
 Ser Val Pro Val Ser Glu Arg Arg Ser Val Ala Glu Ser Ile Asp Phe
 1 5 10 15

His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly
 20 25 30

Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys
 35 40 45

Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
 50 55 60

Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
 65 70 75 80

Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe

85	90	95
Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu		
100	105	110
Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser		
115	120	125
Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser		
130	135	140
Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys		
145	150	155
Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe		
165	170	175
Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val		
180	185	190
Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp		
195	200	205
Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro		
210	215	220
Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro		
225	230	235
240		
Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly		
245	250	255
Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu		
260	265	270
Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp		
275	280	285
Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met		
290	295	300
Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro		
305	310	315
320		
Asn Ile Val Thr Phe Ser Ala Val Pro His Pro Asp Val Lys Pro Met		
325	330	335
Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn		
340	345	

<210> 15
<211> 1041
<212> DNA
<213> Arabidopsis thaliana

<400> 15

gtgccagtat	ctgaaaggcg	ttcagtagct	gagtccattg	acttccatac	aatagaggtt	60
gagccacaat	attctggtgc	tagaatttag	ggagaggaag	ttaccttaga	ttttgtgaaa	120
acgatgatgg	aggatttaa	gaaccaaaaa	acattgcata	aacggtatgc	ctatcaaatc	180
gtcttacaga	ctaggcaaat	cttgcttagca	ctgccttctc	ttgttgatat	aagtgttcca	240
catggcaaac	atatcactgt	ttgcggtgac	gttcatggtc	agttctacga	tcttctcaat	300
atctttgagc	ttaatggcct	cccttcggag	gagaaccat	acctattaa	tggcgacttt	360
gtggacagag	gctcattctc	cgttgagatc	atcctcaett	tgtttgctt	caagtgcatg	420
tgcccattcat	ccatatatct	agccagagga	aaccatgaaa	gcaagagcat	gaacaaaatt	480
tatggttttg	agggtgaggt	tccgtccaag	ttgagtgaaa	aattcgtgga	tctctttgct	540
gaagttttct	gttacccccc	gttggctcat	gttataaatg	ggaaggctt	cgtggtacat	600
ggaggtctt	tcagtggtga	cggcgtgaaa	ctctcagaca	tcagagccat	tgacagattc	660
tgtgagccac	cagaggaagg	actaatgtgt	gaactattgt	ggagtgatcc	tcaacctctc	720
ccttggaaagag	gcccaagcaa	gcgaggagtt	ggtctatcat	ttggtgggaga	tgtgacaaag	780
aggtttttgc	aagataacaa	tttagatttg	ttggtccggt	cacatgaagt	aaaagatgaa	840
ggttatgagg	ttgaacatga	cggtaaactc	ataactgtct	tctctgcgcc	aaattactgt	900
gatcagatgg	gtaataaggg	agccttcatt	cgtttgaag	ctcctgatat	gaagccaaac	960
attgttacat	tctcagcagt	gcctcatccg	gatgtgaagc	ctatggcata	tgcaaacaac	1020
tttctcagga	tgttcaacta	a				1041

<210> 16
<211> 479
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)
<223> PAPP5

<400> 16
Met Glu Thr Lys Asn Glu Asn Ser Asp Val Ser Arg Ala Glu Glu Phe
1 5 10 15

Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
20 25 30

Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95

Glu Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Gly Leu Ser Pro
100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
225 230 235 240

Glu Asp Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
260 265 270

Phe Ala Glu Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys
355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
420 425 430

Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg
435 440 445

Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val
450 455 460

Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn
465 470 475

<210> 17

<211> 492

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)

<223> PP5

<400> 17

Glu Arg Thr Glu Cys Ala Glu Pro Pro Arg Asp Glu Pro Pro Ala Asp
1 5 10 15

Gly Ala Leu Lys Arg Ala Glu Glu Leu Lys Thr Gln Ala Asn Asp Tyr
20 25 30

Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala
35 40 45

Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu
50 55 60

Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr
65 70 75 80

Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg
85 90 95

Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp

100

105

110

Tyr Glu Thr Val Val Lys Val Lys Pro